IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Florian LANG et al.

Title: CELL VOLUME-REGULATED HUMAN KINASE H-SGK

Prior Appl. No.: 09/031,295

Prior Appl. Filing Date: 02/26/1998

Examiner: unassigned

Art Unit: unassigned

PRELIMINARY AMENDMENT

Commissioner for Patents
Box PATENT APPLICATION
Washington, D.C. 20231

Sir:

Prior to examination of the present Continuing Application, Applicant respectfully requests that the application be amended as follows:

In the Specification:

Please amend the specification as follows:

On page 1, after the Application Title, please add the following paragraph:

This is a Divisonal Application of Application No. 09/031,295, filed 02/26/1998.

On page 1, line 2 add the following title:

Background of Invention

On page 10, line 17 add the following paragraph:

Brief Description of the Drawings

Figures 1A-1E disclose the nucleotide sequence encoding the human cell volume-regulated kinase h-sgk. This sequence corresponds to SEQ ID NO: 1 in the sequence listing.

Figures 2A-2C disclose the amino acid sequence of the human cell volume-regulated kinase h-sgk. This sequence corresponds to SEQ ID NO: 2 in the sequence listing.

On page 10, delete line 18, and replace with the following in accordance with 37 CFR §1.121. A marked up version showing changes is attached:

Detailed Description of the Invention

On page 14, delete the 1st full paragraph, and replace with the following in accordance with 37 CFR §1.121. A marked up version showing changes is attached:

Nucleotide sequence accession number: The h-sgk cDNA sequence, SEQ ID NO:1, was entered into the GenBank database under accession number Y10032 and was inaccessible until March 27, 1997.

On page 15, delete 1st full paragraph, lines 9-13, and replace this paragraph with the following in accordance with 37 CFR §1.121. A marked up version showing changes is attached:

A single transcript of about 2.6 kilobases was greatly influenced by the changes in the extracellular osmolarity (Figs. 1A-1E). The amount of transcript was reduced when the osmolarity decreased and was enhanced when the osmolarity increased.

On page 16, delete 1st full paragraph, lines 8-31, and replace this paragraph with the following in accordance with 37 CFR §1.121. A marked up version showing changes is attached:

The Genbank database was scanned for similar human sequences using the FASTA computer program. Several EST (Expressed Sequence Tags) DNA sequences from the TIGR/ATCC special collection of human cDNA clones showed 100% sequence agreement with parts of the h-sgk cDNA fragments. After multiple alignments of 30 different TIGR/ATCC human cDNA clones with the rat sgk cDNA sequence (Genbank accession number L01624) and with the h0sgk DNA fragment, it was assumed that the I.M.A.G.E. consortium construct with the clone ID 42669 from a human infantile brain library has the complete coding sequence of the h-sgk. Sequence analysis of this

construct with coinciding sequences in th sense and antisense directions revealed a cDNA sequence of about 2.4 kilobases. In order to demonstrate involvement of the complete h-sgk, the 5' end of the clone (nucleotides 1-285 of the coding sequence) was subcloned into the pCR II vector and hence a new probe was produced with this construct. Hybridization of a Northern blot with this probe resulted in identical results as with the original probes (Figs. 1A-1E). The longest reading frame in the clone investigated (1.3 kb) afforded a 431 amino acid protein with an overall identity of 98% with the rat sgk protein.

On page 25, delete the paragraph starting on line 28 and ending on page 26, line 7, and replace with the following in accordance with 37 CFR §1.121. A marked up version showing changes is attached:

Detailed of antibody production: The rabbits were immunized by using two peptides from the h-sgk amino acid sequence: Pos. 386-Pos. 404 (DPEFTEEPVPNSIGKSPDS), Pos. 416-Pos. 431 (EAFLGFSYAPPTDSFL). The two peptides (SEQ ID NOS 3 and 4, respectively) were conjugated to KLH and to MAP, respectively, as carrier and injected intracutaneously with complete and incomplete, respectively, Freund's adjuvant. The injection and blood-sampling protocol followed standard procedures. The immune sera were purified by affinity chromatography, and the antibody fractions were collected and used at a concentration of about 1 mg/ml.

On page 27, at the end of the specification, before the claims, insert the printed Sequence Listing submitted concurrently herewith.

In the Claims:

Please renumber pages 28-32 as pages 33-37 respectively.

Please cancel claims 1-20.

Please add the following new claims:

21. An isolated nucleic acid coding for the human cell volume-regulated kinase (h-sgk) comprising the amino acid sequence shown in SEQ ID NO:2 or a fragment thereof.

22. An isolated nucleic acid comprising the nucleotide sequence shown in SEQ ID NO:1 or a fragment thereof.

23. An isolated nucleic acid which hybridizes with the nucleic acid as claimed in claim 21 under stringent conditions and which codes for a functionally active cell volume-regulated kinase whose transcription can be induced neither by fetal calf serum (FCS) nor by a glucocorticoid.

24. An isolated nucleic acid which hybridizes with the nucleic acid as claimed in claim 22 under stringent conditions and which codes for a functionally active cell volume-regulated kinase whose transcription can be induced neither by fetal calf serum (FCS) nor by a glucocorticoid.

25. An isolated nucleic acid which hybridizes with the nucleic acid as claimed in claim 21 under stringent conditions and which codes for a functionally active cell volume-regulated kinase which is not identical to rat sgk.

26. An isolated nucleic acid which hybridizes with the nucleic acid as claimed in claim 22 under stringent conditions and which codes for a functionally active cell volume-regulated kinase which is not identical to rat sgk.

27. A nucleic acid fragment encoding an amino acid sequence comprising approximately the region of amino acid position 313 to 431 of the amino acid sequence as claimed in claim 21.

28. A nucleic acid fragment comprising approximately the region of nucleotide position 980 to 1480 of the nucleic acid sequence as claimed in claim 22.

29. A nucleic acid fragment coding for an immunologically active fragment of the human cell volume-regulated kinase h-sgk.

30. A nucleic acid fragment as claimed in claim 29 coding for a fragment comprising at least one of the following amino acid sequences:

DPEFTEEPVPNSIGKSPDS (SEQ ID. NO: 3)

EAFLGFSYAPPTDSFL (SEQ ID NO: 4)

31. A nucleic acid fragment as claimed in claim 29 coding for a fragment consisting of at least one of the following amino acid sequences:

DPEFTEEPVPNSIGKSPDS (SEQ ID. NO: 3)

EAFLGFSYAPPTDSFL (SEQ ID. NO: 4)

32. A pharmaceutical composition comprising the nucleic acid as claimed in claim 21.

33. A pharmaceutical composition comprising the nucleic acid as claimed in claim 22.

34. A pharmaceutical composition comprising the nucleic acid as claimed in claim 27.

35. A pharmaceutical composition comprising the nucleic acid as claimed in claim 28.

36. A pharmaceutical composition comprising the nucleic acid as claimed in claim 29.

37. A pharmaceutical composition comprising the nucleic acid as claimed in claim 30.

38. A pharmaceutical composition comprising the nucleic acid as claimed in claim 31.

REMARKS

Applicant respectfully requests that the foregoing amendments be made prior to examination of the present application.

After amending the claims as set forth above, claims 21-38 are now pending in this application. The pending claims are fully supported by the specification and original claims. Claims 27 and 28 specifically have support in the specification on page 25, line 16 that recites the nucleotide fragment of nucleotides 980-1480. Reference to SEQ ID NO: 1 shows both the nucleotide and corresponding amino acid sequences. From a review of these sequences, it is noted that nucleotide 980 is the second nucleotide of the codon that encodes amino acid 313, i.e., Pro. Nucleotide 1480 is in the 3' non-coding region, and therefore, the nucleotide fragment; i.e., nucleotides 980-1480 encodes the amino acid sequence that ends at amino acid 431, Leu, the last amino acid of SEQ ID NO: 2. Thus, claim 27 claims the nucleic acid fragment the encodes the corresponding fragment of the amino acid sequence.

Applicants submit this Preliminary Amendment to insert required references to SEQ ID NOS of the Sequence Listing filed concurrently herewith, to indicate the insertion point for the Sequence Listing, and to effect the necessary changes in pagination. No new matter is added.

Applicant believes that the present application is now in condition for allowance. Favorable consideration of the application as amended is respectfully requested.

The Examiner is invited to contact the undersigned by telephone if it is felt that a telephone interview would advance the prosecution of the present application.

Respectfully submitted,

Date Dec 4, 2001

By

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Marked-up Version of Specification:

Page 10, line 18:

[Detailed description of the invention] **Detailed Description of the Invention**

Page 14, 1st full paragraph:

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Page 15, 1st full paragraph, lines 9-13:

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